

AMENDMENTS TO THE CLAIMS

1. **(Currently Amended)** A method for identifying an eRNA or a DNA Sequence comprising an eRNA-encoding sequence in the nucleome of a eukaryotic cell, said method comprising:

identifying non-protein-encoding nucleotide sequences within an RNA transcript or a DNA sequence encoding ~~same~~ said non-protein-encoding nucleotide sequences in said nucleome;

determining the nucleotide sequence of said non-protein-encoding nucleotide sequence; and ~~subjecting said sequence to phenotyping to determine its effect on one or more biological events within a cell and/or~~

determining the degree to which said sequence is conserved in the cell's genome or in the genome of other species or genera of eukaryotic cells, wherein a non-protein-encoding nucleotide sequence ~~having a biological effect in a cell or a nucleotide sequence~~ conserved within the genome or between different cells' nucleomes is deemed to be an eRNA or DNA sequence comprising a nucleotide sequence encoding ~~same~~ said eRNA.

2. **(Currently Amended)** A method for identifying a receiver DNA or RNA sequence, said method comprising:

identifying non-protein-encoding nucleotide sequences within an RNA transcript or a DNA sequence encoding ~~same~~ said non-protein-encoding nucleotide sequences in said nucleome;

determining the nucleotide sequence of said non-protein-encoding nucleotide sequence; and ~~subjecting said sequence to phenotyping to determine its effect on one or more biological events within a cell and/or~~

determining the degree to which said sequence is conserved in the cell's genome or in the genome of other species or genera of eukaryotic cells wherein a non-protein-encoding nucleotide sequence ~~having a biological effect in a cell or a nucleotide sequence~~ conserved within the genome or between different cells' nucleomes is deemed to be an eRNA or DNA sequence comprising a nucleotide sequence encoding ~~same~~ said eRNA; and then

contacting said eRNA with nucleome and proteome material; and

screening for interaction between the eRNA and ~~an~~ a DNA or RNA in the nucleome material, or a protein expressed by said DNA or RNA in the proteome material, wherein the detection of such an interaction is indicative of the DNA or RNA being a receiver molecule.

3. **(Currently Amended)** The method of Claim 1 or 2 wherein the determining the degree to which said sequence is conserved ~~phenotyping~~ comprises determining the degree to which a non-protein-encoding sequence is conserved within a cell's genome.

4. **(Currently Amended)** The method of Claim 1 or 2 ~~or 3~~ wherein the determining the degree to which said sequence is conserved ~~phenotyping~~ comprises determining the degree to which a non-protein-encoding sequence is conserved amongst genomes of different species, genera or families.

5. **(Canceled)**

6. **(Original)** The method of Claim 1 or 2 wherein the eRNA is or is derived from an intron.

7. **(Original)** The method of Claim 1 or 2 wherein the eRNA is or is derived from an exon.

8. **(Original)** The method of Claim 2 wherein the receiver DNA or RNA is located in the coding sequence of a gene or its RNA transcript, in the 3' or 5' flanking region of a gene or its RNA transcript, in the intron or intron-exon junction of a gene or its RNA transcript, or in an intergenic (non transcribed) region of the genome.

9. **(Original)** The method of Claim 1 or 2 wherein the eukaryotic cell is from a vertebrate.

10. **(Original)** The method of Claim 1 or 2 wherein the eukaryotic cell is from an invertebrate.

11. **(Original)** The method of Claim 1 or 2 wherein the vertebrate is a mammal.

12. **(Original)** The method of Claim 1 or 2 wherein the vertebrate is an avian species.

13. **(Original)** The method of Claim 1 or 2 wherein the vertebrate is a reptilian species.

14. **(Original)** The method of Claim 1 or 2 wherein the vertebrate is an amphibian species.

15. **(Original)** The method of Claim 1 or 2 wherein the mammal is a human.

16. **(Original)** The method of Claim 1 or 2 wherein the eukaryotic cell is from a plant.
17. **(Original)** The method of Claim 1 or 2 wherein the plant is a monocotyledonous plant.
18. **(Original)** The method of Claim 1 or 2 wherein the plant is a dicotyledonous plant.
19. **(Currently amended)** A method for identifying a receiver protein, said method comprising:

identifying non-protein-encoding nucleotide sequences within an RNA transcript or a DNA sequence encoding ~~same~~ said non-protein-encoding nucleotide sequences in said nucleome;

determining the nucleotide sequence of said non-protein-encoding nucleotide sequence; ~~and subjecting said sequence to phenotyping to determine its effect on one or more biological events within a cell and/or~~

determining the degree to which said sequence is conserved in the cell's genome or in the genome of other species or genera of eukaryotic cells wherein a non-protein-encoding nucleotide sequence ~~having a biological effect in a cell or a nucleotide sequence~~ conserved within the genome or between different cells' nucleomes is deemed to be an eRNA or DNA sequence comprising a nucleotide sequence encoding ~~same~~ said eRNA; ~~and then~~

contacting said eRNA with proteome material; and

screening for interaction between the eRNA and a protein in the proteome material, wherein the detection of such an interaction is indicative of a receiver protein.

20. **(Currently Amended)** The method of Claim 19 wherein the determining the degree to which said sequence is conserved ~~phenotyping~~ comprises determining the degree to which a non-protein-encoding sequence is conserved within a cell's genome.

21. **(Currently Amended)** The method of Claim 19 wherein the determining the degree to which said sequence is conserved ~~phenotyping~~ comprises determining the degree to which a non-protein-encoding sequence is conserved amongst genomes of different species, genera or families.

22. **(Canceled)**

23. **(Original)** The method of Claim 19 wherein the eRNA is an intron.

24. **(Original)** The method of Claim 19 wherein the eRNA is an exon.

25. **(Original)** The method of Claim 19 wherein the eukaryotic cell is from a vertebrate.
26. **(Original)** The method of Claim 19 wherein the eukaryotic cell is from an invertebrate.
27. **(Currently Amended)** The method of Claim 25 19 wherein the vertebrate is a mammal.
28. **(Currently Amended)** The method of Claim 25 19 wherein the vertebrate is an avian species.
29. **(Currently Amended)** The method of Claim 25 19 wherein the vertebrate is a reptilian species.
30. **(Currently Amended)** The method of Claim 25 19 wherein the vertebrate is an amphibian species.
31. **(Currently Amended)** The method of Claim 27 19 wherein the mammal is a human.
32. **(Original)** The method of Claim 19 wherein the eukaryotic cell is from a plant.
33. **(Currently Amended)** The method of Claim 32 19 wherein the plant is a monocotyledonous plant.
34. **(Currently Amended)** The method of Claim 32 19 wherein the plant is a dicotyledonous plant.
35. **(Original)** A method of modulating the phenotype of a cell, said method comprising identifying an eRNA associated with the particular phenotype by the method of Claim 1 or a receiver sequence for the eRNA by the method of Claim 2 or 19 and manipulating the cell to up-or down-regulate the level or activity of the eRNA or its receiver sequence to thereby alter the phenotype of the cell.
36. **(Currently amended)** The method of claim 35 3-5 wherein the eRNA is derived from an intron.
37. **(Currently amended)** The method of claim 35 3-8 wherein the eRNA is derived from an exon.
38. **(Currently amended)** The method of claim 35 3-8 wherein the receiver DNA is RNA is is located in the coding sequence of a gene or its RNA transcript, in the 3' or 5' flanking

region of a gene or its RNA transcript, in the intron or intron-exon junction of a gene or its RNA transcript, or in an intergenic (non transcribed) region of the genome.

39. **(Original)** The method of claim 35 wherein the eukaryotic cell is for a vertebrate,

40. **(Original)** The method of claim 35 wherein the eukaryotic cell is from an invertebrate.

41. **(Currently Amended)** The method of claim 35 39 wherein the vertebrate is a mammal.

42. **(Currently Amended)** The method of claim 35 39 wherein the vertebrate is an avian species.

43. **(Currently Amended)** The method of claim 35 39 wherein the vertebrate is a reptilian species.

44. **(Currently Amended)** The method of Claim 35 39 wherein the vertebrate is an amphibian species.

45. **(Currently Amended)** The method of Claim 35 41 wherein the mammal is a human.

46. **(Original)** The method of Claim 35 wherein the eukaryotic cell is from a plant.

47. **(Currently Amended)** The method of Claim 35 46 wherein the plant is a monocotyledonous plant.

48. **(Currently Amended)** The method of Claim 35 46 wherein the plant is a dicotyledonous plant.

49-52. **(Canceled)**

53. **(Currently Amended, Withdrawn)** An cRNA molecule identified by the method comprising :

identifying non-protein-encoding nucleotide sequences within an RNA transcript or a DNA sequence encoding ~~same~~ said non-protein-encoding nucleotide sequences in said nucleome;

determining the nucleotide sequence of said non-protein-encoding nucleotide sequence; and ~~subjecting said sequence to phenotyping to determine its effect on one or more biological events within a cell and/or~~

determining the degree to which said sequence is conserved in the cell's genome or in the genome of other species or genera of eukaryotic cells wherein a non-protein-

encoding nucleotide sequence ~~having a biological effect in a cell or a nucleotide sequence~~ conserved within the genome or between different cells' nucleomes is deemed to be an eRNA or DNA sequence comprising a nucleotide sequence encoding ~~same~~ said eRNA.

54. **(Currently Amended, Withdrawn)** A receiver DNA or RNA identified by the method comprising:

identifying non-protein-encoding nucleotide sequences within an RNA transcript or a DNA sequence encoding ~~same~~ said non-protein-encoding nucleotide sequences in said nucleome;_i

determining the nucleotide sequence of said non-protein-encoding nucleotide sequence; ~~and subjecting said sequence to phenotyping to determine its effect on one or more biological events within a cell and/or~~

determining the degree to which said sequence is conserved in the cell's genome or in the genome of other species or genera of eukaryotic cells wherein a non-protein-encoding nucleotide sequence ~~having a biological effect in a cell or a nucleotide sequence~~ conserved within the genome or between different cells' nucleomes is deemed to be an eRNA or DNA sequence comprising a nucleotide sequence encoding ~~same~~ said eRNA; ~~and then~~

contacting said eRNA with nucleome and proteome material; and

screening for interaction between the eRNA and an a DNA or RNA in the nucleome material, or a protein expressed by said DNA or RNA in the proteome material, wherein the detection of such an interaction is indicative of the DNA or RNA being a receiver molecule.

55. **(Currently Amended, Withdrawn)** A receiver protein identified by the method comprising:

identifying non-protein-encoding nucleotide sequences within an RNA transcript or a DNA sequence encoding ~~same~~ said non-protein-encoding nucleotide sequences in said nucleome;_i

determining the nucleotide sequence of said non-protein-encoding nucleotide sequence; ~~and subjecting said sequence to phenotyping to determine its effect on one or more biological events within a cell and/or~~

determining the degree to which said sequence is conserved in the cell's genome or in the genome of other species or genera of eukaryotic cells wherein a non-protein-encoding nucleotide sequence ~~having a biological effect in a cell or a nucleotide sequence~~ conserved within the genome or between different cells' nucleomes is deemed to be an eRNA or DNA sequence comprising a nucleotide sequence encoding same said eRNA; and then

contacting said eRNA with proteome material; and
screening for interaction between the eRNA and a protein in the proteome material, wherein the detection of such an interaction is indicative of a receiver protein.

56. **(Currently Amended, Withdrawn)** A method of inducing post transcriptional gene silencing (PTGS) in a eukaryotic cell, said method comprising identifying an eRNA according to the method of Claim 1, said eRNA having a receiver sequence in a target gene to be silenced, and expressing a DNA comprising said eRNA in said cell for a time and under conditions sufficient for the target gene to be silenced.

57. **(Withdrawn)** The method of claim 56 wherein the cell is a plant cell.
58. **(Withdrawn)** The method of claim 56 wherein the cell is a mammalian cell.
59. **(Withdrawn)** The method of claim 58 wherein the mammalian cell is a human cell.

60. **(Canceled)**

61. **(Original)** A method for detecting an altered genetic network said method comprising screening for the presence or absence of an eRNA or an altered level of eRNA wherein an alteration in the presence, absence or level of eRNA is indicative of an altered genetic network and thereby an altered phenotype.